

NEB 1233

	-1391	-1381	-1371	-1361	-1351	-1341	-1331	-1321
	*	*	*	*	*	*	*	*
	AGCGGATAAC AATTTCACAC AGGAAACAGC TATGACCATG ATTACGCCAA GOTTGGTACC GAGCTCGGAT CCACTAGTAA							
	pCR2.1 -BamHI-							
	Lac promoter >							
	-1311	-1301	-1291	-1281	-1271	-1261	-1251	-1241
	*	*	*	*	*	*	*	*
	CGGCCGCCAG TGTGCTGGAA TTCGGCTTAC TATAGGGCAC GCGTGGTCGA CGGCCCGGGC TGGTAACTTT AAGAGAAATT							
	pCR2.1 -SmaI-							
	GenomeWalker Adaptor >							
	cmAC01 >							
	-1231	-1221	-1211	-1201	-1191	-1181	-1171	-1161
	*	*	*	*	*	*	*	*
	GGTAAATTC CTAGAGAGAA TTGTAATTAA TATAGGAGAA TGATTTTAAAT TCTAATGTTG TATCCATTTT CGATAAAGTT							
	cmAC01 Genomic DNA >							
	-1151	-1141	-1131	-1121	-1111	-1101	-1091	-1081
	*	*	*	*	*	*	*	*
	AAATAAAGTG TCGTAGACGA CCATCATCTT TAATCCATTT GTACTTAICA AATTGTATC TGAGATTTAA GTTCAAATTC							
	cmAC01 Genomic DNA >							
	-1071	-1061	-1051	-1041	-1031	-1021	-1011	-1001
	*	*	*	*	*	*	*	*
	ACACTAAAC AATCGAAATG TATGCGACAA TCACAATGA AAATACGTAT GATGTATTC ATCACCTTTC AAGTTCTAAC							
	cmAC01 Genomic DNA >							
	-991	-981	-971	-961	-951	-941	-931	-921
	*	*	*	*	*	*	*	*
	CTAGGATATG TTTTGAATA TTTGAGATTT ATTAAATTAT TCTTTTATCC GTTGACAGTT TATTTTTTGT TTAACGATGT							
	cmAC01 Genomic DNA >							
	-911	-901	-891	-881	-871	-861	-851	-841
	*	*	*	*	*	*	*	*
	ATGTAAGAAA CGACGAAATA TGTGATTAAA CCAAGATCGC ATACAAATAA GAGCTAGATC CTAAAGATAT ATAAAAGTAT							
	cmAC01 Genomic DNA >							
	-831	-821	-811	-801	-791	-781	-771	-761
	*	*	*	*	*	*	*	*
	GATCAACAAC GTACAAAACG TTTCTTTTCG ATGATAATTA TCTTAAGAAC TTCAAGGTTA ATTTAGATCT CTTAATTAAA							
	cmAC01 Genomic DNA >							
	-751	-741	-731	-721	-711	-701	-691	-681
	*	*	*	*	*	*	*	*
	AAATTTTATA GATAATGCAT CCGTGAACAA GAAAAACAT AAAGAACCCA TGGTTGTCCT AATTTTGTGA GTAAATAAGC							
	cmAC01 Genomic DNA >							
-671	-661	-651	-641	-631	-621	-611	-601	
	*	*	*	*	*	*	*	*
	GTAGTTCAAG ACACAAGTAA GAATGACGTT ACCCATGTT AATCTAGATT CCAAACTTG AGCTTGAGAG CAOGTTACGA							
	cmAC01 Genomic DNA >							

Fig. 1A

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-591      -581      -571      -561      -551      -541      -531      -521
  *        *        *        *        *        *        *        *
AAATAATCTA CGAAAACGAG TAAGTCGTCT AAGTTCGTTT TCGTTTATTT GACACGTAAG ATACTCGTAT TGAAAGAAGA
cmAC01 Genomic DNA>

-511      -501      -491      -481      -471      -461      -451      -441
  *        *        *        *        *        *        *        *
CGAAAAATGG AAAAAAGTAA AGAAGGTAAG GAGGTGGGTG AGTCCAAAGG AAACATACCA AATTCATGCA AGAACTATGA
cmAC01 Genomic DNA>

-431      -421      -411      -401      -391      -381      -371      -361
  *        *        *        *        *        *        *        *
GATTCAGAAA TTAAGAGAAA AGTGTGGAAA TCATGTAAGT AAATTTAAAA TACATATAGG TACTATTTTC TTTCCTTTTC
cmAC01 Genomic DNA>

-351      -341      -331      -321      -311      -301      -291      -281
  *        *        *        *        *        *        *        *
TATTGAAACA AAGAGACCAA GGGGGAATTA GGGTATATGG CATTGGCAGA CATAAAAATA ATAAAGTTAA ATCAAATTGG
cmAC01 Genomic DNA>

-271      -261      -251      -241      -231      -221      -211      -201
  *        *        *        *        *        *        *        *
GTCCCAAAC TACCAAGAG GAAATTCAGT GTTGAATAAA GCCAATTAGC CAAAGCCAAA GOCAAAGCCA CCTCCTCTCT
cmAC01 Genomic DNA>

-191      -181      -171      -161      -151      -141      -131      -121
  *        *        *        *        *        *        *        *
TTCCACATA CATGCATGAA ATTTTCATGG OCCATTCITT TTATCATCAC ATTTTAAATA ATTTATCIT CTCTCTCTC
cmAC01 Genomic DNA>

-111      -101      -91      -81      -71      -61      -51      -41
  *        *        *        *        *        *        *        *
TTCTCTCTCT TCTTCTCTT CTCTCTCTC TTCTCTCTCT TTTTTAATC AATTTCITCC CACTTCCAA TCCTAAATAA
cmAC01 Genomic DNA>

TATA box
|
-31      -21      -11      -1      10      20      30      40
  *        *        *        *        *        *        *        *
ATTTCACTAT AAATACCCCT TCATTATAAC TTGATCCAAC ACACCCACCA ACCAAAAACA AAACCTTGAT ACCAAAGAGT
cmAC01 Genomic DNA>

50      60      70      80      90      |
  *        *        *        *        *        |
TCTTTTTTCT TTATTTCAC AAACCAAATC TTGTATCTAC AAAAAGAAAT GGCTGTCTA
TAG AACATAGATG TTTTCTTcc taGgCAGAT
-BamHI-
cmAC01 Genomic DNA

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Fig. 1B

-1289	-1279	-1269	-1259	-1249	-1239	-1229	-1219
*	*	*	*	*	*	*	*
AGGAAACAGC	TATGACCATG	ATTACGCCAA	GCTTAAGAGA	AATTGGTAAA	ATTCTAGAG	AGAATTGTAA	TTAATATAGG
HindIII							
pUC19				cmACO1 Genomic DNA			
-1209	-1199	-1189	-1179	-1169	-1159	-1149	-1139
*	*	*	*	*	*	*	*
AGAATGATT	TAATTCTAAT	GTTGTATCCA	TTTTCGATAA	AGTTAAATAA	AGTGTCTAG	ACGACCATCA	TTCTTAATCC
cmACO1 Genomic DNA							
-1129	-1119	-1109	-1099	-1089	-1079	-1069	-1059
*	*	*	*	*	*	*	*
ATTGTACTT	ATCAAATTG	TATCTGAGAT	TTAAGTTCAA	ATTCACACTA	AAACAATCGA	AATGTATGCG	ACAATCACAA
cmACO1 Genomic DNA							
-1049	-1039	-1029	-1019	-1009	-999	-989	-979
*	*	*	*	*	*	*	*
TGGAAAATAC	GTATGATGTA	TTCCATCACC	TTTCAAGTTC	TAACCTAGGA	TATGTTTTGG	AATATTGAG	ATTATATTAA
cmACO1 Genomic DNA							
-969	-959	-949	-939	-929	-919	-909	-899
*	*	*	*	*	*	*	*
TTATTCTTTT	ATCGTTGAC	AGTTTATTTT	TTGTTTAACG	ATGTAATGTA	GAAACGACGA	AATATGTGAT	TAAACCAAGA
cmACO1 Genomic DNA							
-889	-879	-869	-859	-849	-839	-829	-819
*	*	*	*	*	*	*	*
TOGCATACAA	ATAAGAGCTA	GATCCTAAAG	ATATATAAAA	GTATGATCAA	CAACGTACAA	AACGTTTCTT	TTTCATGATA
cmACO1 Genomic DNA							
-809	-799	-789	-779	-769	-759	-749	-739
*	*	*	*	*	*	*	*
ATTATCTTAA	GAACCTCAAG	GTTAATTTAG	ATCTCTTAAT	TAAAAAATTT	CATAGATAAT	GCATCCGTGA	ACAAGAAAAA
cmACO1 Genomic DNA							
-729	-719	-709	-699	-689	-679	-669	-659
*	*	*	*	*	*	*	*
ACATAAAGAA	CCCATGGTTG	TCCTAATTTT	TGTAGTAAAT	AAGCGTAGTT	CAAGACACAA	GTAAGAATGA	CGTTACCACA
cmACO1 Genomic DNA							
-649	-639	-629	-619	-609	-599	-589	-579
*	*	*	*	*	*	*	*
TGTTAATCTA	GATTCCAAAA	CTTGAGCTTG	AGAGCACGTT	ACGAAAATAA	TCTACGAAAA	CGAGTAAGTC	GTCTAAGTTC
cmACO1 Genomic DNA							
-569	-559	-549	-539	-529	-519	-509	-499
*	*	*	*	*	*	*	*
GTTTTCGTTT	ATTTGACACG	TAAGATACTC	GTATTGAAAG	AAGACGAAAA	ATGGAAAAAA	GTAAAGAAGG	TAAGGAGGTG
cmACO1 Genomic DNA							

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-489      -479      -469      -459      -449      -439      -429      -419
  *        *        *        *        *        *        *        *
GGTGAGTCCA AAGGAAACAT ACCAAATTCA TGCAAGAAGT ATGAGATTCA GAAATTAAGA GAAAAGTGTG GAAATCATGT
cmAC01 Genomic DNA>

-409      -399      -389      -379      -369      -359      -349      -339
  *        *        *        *        *        *        *        *
AACTAAATTT AAAATACATA TAGGTACTAT TTTCTTTCCT TTTCTATTGA AASRAAGAGA NNAAGGGGGA ATTAGNGTAT
cmAC01 Genomic DNA>

-329      -319      -309      -299      -289      -279      -269      -259
  *        *        *        *        *        *        *        *
ATGGCATTGG CAGACATAAA AATAATAAAG TTAAATCAAA TTGGGTCCCA AACTCACCAA AGAGGAAATT CAGTGTGTAA
cmAC01 Genomic DNA>

-249      -239      -229      -219      -209      -199      -189      -179
  *        *        *        *        *        *        *        *
TAAAGCCAAT TAGCCAAAGC CAAAGCCAAA GCCACCTCCT CTCTTTTCCA CATACTGCA TGAAATTICA TGGGCCCAT
cmAC01 Genomic DNA>

-169      -159      -149      -139      -129      -119      -109      -99
  *        *        *        *        *        *        *        *
CTTTTATCA TCACATTTT AATAATTTTA TCTTCTCTT CTCTCTCTC TCTTCTCTT TCTTCTCTT CTCTCTCTC
cmAC01 Genomic DNA>

-89      -79      -69      -59      -49      -39      -29      -19
  *        *        *        *        *        *        *        *
TCTTTTCTT AATCAATTC TCCCACTTT CCAATCCTAA ATAAATTICA CTATAAATAC CCCTTCATTA TAACTTGATC
cmAC01 Genomic DNA>
TATA box
|
transcriptional start site in Tomato E4
|
-9      2      12      translational start site
  *      *      *      |
CAACACACCC AGGATCCATT ATTAGAGATT GAGCC ATGG
BamH1
__cmAC01__      __Tom E4 5'UTR__

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Fig. 2B

NEB 1233

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|      -1669      -1659      -1649      -1639      -1629      -1619      -1609      -1599
|      *          *          *          *          *          *          *          *
AGCGGATAAC AATTTACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTTGGTACC GAGCTCGGAT CCACTAGTAA
                                     HindIII      -BamHI-
_____ Lac promoter _____>
_____ pCR2.1 _____>

      -1589      -1579      -1569      -1559      -1549      -1539      -1529      -1519
      *          *          *          *          *          *          *          *
CGGCCGCCAG TGTCGTGGAA TTCGGCTTGT AATACGACTC ACTATAGGGC ACGCGTGGTC CACGGCCCGG GCTGGTAACT
_____ pCR2.1 _____>
_____ GenomeWalker Adaptor _____>

      -1509      -1499      -1489      -1479      -1469      -1459      -1449      -1439
      *          *          *          *          *          *          *          *
AGAAGCTAAA GGACGACGTC AACATAATTA AAATTACTCC AAGATAATTA AAATTAAAAA TATCTTATAT TTTATGGCGT
_____ MEL7 promoter _____>

      -1429      -1419      -1409      -1399      -1389      -1379      -1369      -1359
      *          *          *          *          *          *          *          *
TACATCTTCC TTTCCTCTTC TTCTTTTTTC TGCTGCGATT TCTTCOCATC TATTCTCTCT TTTACTCTTA TTTTTTCTT
_____ MEL7 promoter _____>

      -1349      -1339      -1329      -1319      -1309      -1299      -1289      -1279
      *          *          *          *          *          *          *          *
TACATGTGTT AGATTGGGT AACCAAATCT GATTCTTTC TATCGICTTT CTCTTTTTTC TCTTTTTTTT TCGCTGCGA
_____ MEL7 promoter _____>

      -1269      -1259      -1249      -1239      -1229      -1219      -1209      -1199
      *          *          *          *          *          *          *          *
TTTCTTCCCA TTGCTATATG TTTTTTCCTC TTTTTTTTTT TACATCGTAA CCAAATCTAA AAGATCGTAT ATAAAGAATC
_____ MEL7 promoter _____>

      -1189      -1179      -1169      -1159      -1149      -1139      -1129      -1119
      *          *          *          *          *          *          *          *
TTCAAAAAAA AAAATTGTTT AGATTGGAGT AGCCAAATTT AAACAATCGC GTAAAAAATA TAAACGATCG TAGACAAATC
_____ MEL7 promoter _____>

      -1109      -1099      -1089      -1079      -1069      -1059      -1049      -1039
      *          *          *          *          *          *          *          *
TAAACGATCG TGCACAAAAA GATTTAAAAA AATCGTTTAG TCAAATCTAA ACAATTGTAT AACCAAATTA AACGATAGAA
_____ MEL7 promoter _____>

      -1029      -1019      -1009      -999      -989      -979      -969      -959
      *          *          *          *          *          *          *          *
TTGAAATAAT AAATCGGTTA GATTGGCTA TCCAAATTTA AATGACCAAA TCTAAACGAT CGTATACCAA ATCTAAACGA
_____ MEL7 promoter _____>

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Fig. 3A


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      -149      -139      -129      -119      -109      -99      -89      -79
      *        *        *        *        *        *        *        *
TGGGTCCTCT TTATCACCCT CATGATAATT ATGAAAAATA AAATAAAATT TAATTATATA ATTCATTCA TCTAATCGTA
_____MEL7 promoter_____>

                        TATA box
      -69      -59      -49      -39      -29      -19      -9      2
      *        *        *        *        *        *        *        *
CAAGCTAGAT ATTACTATAT CAACAACCTT GTGTATAAAA AGGGCAAGAA ATTAAGCATT ATCGTGTGAG CCACTTTTTC
_____MEL7 promoter_____>

                        Mel7 translational start site
                        |
                        |<cmDruNcoSt
                        |
      12      22      32      42      52
      *        *        *        *        *
TATATCTAGA GATAGAAGGT TTAAAATCAT GTCTCTAATT GGAAAGCTTG TGAGT
      TTCCA AATTTTgGTA CcGAGAgTAA CCTTTTCG
                        -NcoI-
_____MEL7 promoter_____>
                        _____MEL7 cds_____>

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Fig. 3C

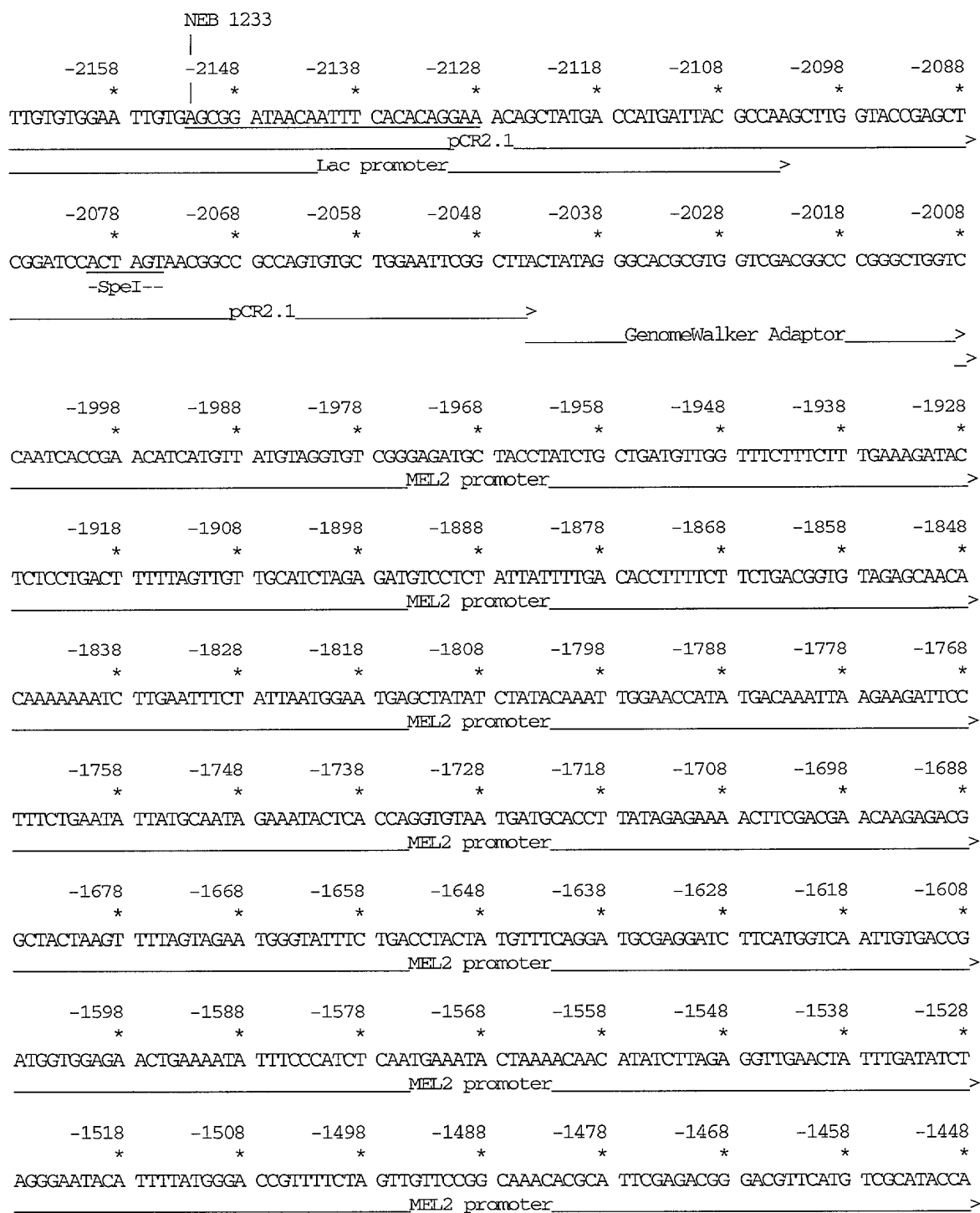


Fig. 4A

-1438 -1428 -1418 -1408 -1398 -1388 -1378 -1368
 * * * * * * * *
 CGGAGGATCC GCATGTAAGC TATCCAAGCA ATACTTCTAC CCTTTTGTTC TTCTTTAATA ATATATTTTT TACTTACTAA
 _____MEL2 promoter_____>

-1358 -1348 -1338 -1328 -1318 -1308 -1298 -1288
 * * * * * * * *
 GATAGTTTCT AAATTTGTTG TAGAATCGAA TGCTGGAAC TCACTCCTAG CTTACCTCAG TGGGTACTTA GCCACTCTCT
 _____MEL2 promoter_____>

-1278 -1268 -1258 -1248 -1238 -1228 -1218 -1208
 * * * * * * * *
 GGGACAAGA TATGCGAGAT GCGGTTGGAT AGACGATTGG ACTACTCAAA AGGCCTTGGT TGGGGACCTA AGTCTAGGGC
 _____MEL2 promoter_____>

-1198 -1188 -1178 -1168 -1158 -1148 -1138 -1128
 * * * * * * * *
 CCACAAGACG GCCAGTGTA GTAGTTCCAC GACCTCATGT TTGTAGTCCA CGGTAGAGCT CCAATTATGG ACTAAGCTTG
 _____MEL2 promoter_____>

-1118 -1108 -1098 -1088 -1078 -1068 -1058 -1048
 * * * * * * * *
 ATCAAGCTGT GCAACGGATT GAAGAACAAA CAAGAAATCA CGATGCGTTA GCTTCAAAAG TGAATGAAT GTGAAAGTTC
 _____MEL2 promoter_____>

-1038 -1028 -1018 -1008 -998 -988 -978 -968
 * * * * * * * *
 ATAGAAGACA TGAGTCGGGC ACAGTAAGGA CCACAACATT ATCTTTAGCT TTGCGATACG TATANNTATT TCCATTATTC
 _____MEL2 promoter_____>

-958 -948 -938 -928 -918 -908 -898 -888
 * * * * * * * *
 TTAAGTTTTT GAATTACAGT ATTCAGTGAT GATATGCATA TATATGTACC AAACGTAGCC ACTTTTGTAT AATTGTAGGA
 _____MEL2 promoter_____>

-878 -868 -858 -848 -838 -828 -818 -808
 * * * * * * * *
 CCTGTGGTGT AGAATGGCAT ATGAGGCTCG TTAAAAGACA TACGATTTC TTGTGCTTT TTITAACGAG GAATATTTT
 _____MEL2 promoter_____>

-798 -788 -778 -768 -758 -748 -738 -728
 * * * * * * * *
 TATTTGTATT ATGAACTTTA TTACATTCT TGAATTCTT TGTATTATGA AGATTTAATT TTTTGTGAA TTTTGTGTTG
 _____MEL2 promoter_____>

-718 -708 -698 -688 -678 -668 -658 -648
 * * * * * * * *
 TATTTTGTA TTTACTAATT TATTTTAAAT TTCTTTAAT TGAATGATA ACGAATGCAA ATATTTTACG AAAAAAAGTT
 _____MEL2 promoter_____>

Fig. 4B

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-638      -628      -618      -608      -598      -588      -578      -568
  *         *         *         *         *         *         *         *
ATAGGAAAAT ATTTCAAAA AATAAAAAAT TACATATTTA AAATATTTTT CGACGCATTA CATATGTGGA AAATATGGTG
MEL2 promoter>

-558      -548      -538      -528      -518      -508      -498      -488
  *         *         *         *         *         *         *         *
CAAACATCAC ATCGGGGATG GTTATTACCG ACGCATGAAT GACACOGAAT ATATAAACGT AAGGAATAGT TATTCTTGAC
MEL2 promoter>

-478      -468      -458      -448      -438      -428      -418      -408
  *         *         *         *         *         *         *         *
GCATACTGCG TGTCGGAACT GTGGAAGTGA GTTCTCGACA TTATTACAC TTACGTGAC GTTTTTATGC ATCGGGAGTC
MEL2 promoter>

-398      -388      -378      -368      -358      -348      -338      -328
  *         *         *         *         *         *         *         *
GCTCCACTTC TTGTAGTGAA GAAATTTTGC CTATAATGTC GGTTTAAAC CGACATTAAA GGCCAAATTT CTCTAGTGC
MEL2 promoter>
Imperfect inverted repeat>

-318      -308      -298      -288      -278      -268      -258      -248
  *         *         *         *         *         *         *         *
ATAATCAATA TMCAAAAGTT CAATTCCTAA AATTACATTT CTCTAGAAAT TCCGTGTGAA CAATTGTCAT AAAGGTTTGA
MEL2 promoter>

-238      -228      -218      -208      -198      -188      -178      -168
  *         *         *         *         *         *         *         *
AGTGAATTGA AAATTTCTAA ACGTAATTGG ATTAAGCGAG AAAATTATTT TAATCACCAT TCAAAAGTTA TTAACAATGA
MEL2 promoter>

-158      -148      -138      -128      -118      -108      -98       -88
  *         *         *         *         *         *         *         *
AAAATATGGA AGATAAGATT TCAAAATTAC GTAATTTACT TCTACGTTTC TTCTTTTCCC CTTTAGTAAC TTCACTCATA
MEL2 promoter>

TATA box
| -78      -68      -58      -48      -38      -28      -18      -8
|  *         *         *         *         *         *         *         *
TCTTTATATA CGTTCATCC CTTACATTC TCATACAAA TTCTCTTTCA ATATCAACTC TCCTCTCTTA ACTCACCTT
MEL2 promoter>

MEL2 translational start site
|      <MEL2_Nco_R
1 3      13      |
* *      *      |
TTTTCAAATG GAAACAATGC AAAC
AAAGggTAC CTTTGTTACG TTG
-NcoI--
pro
MEL2 cds

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Fig. 4C

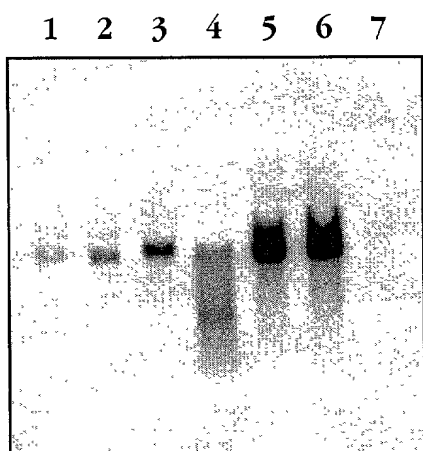


Fig. 5A

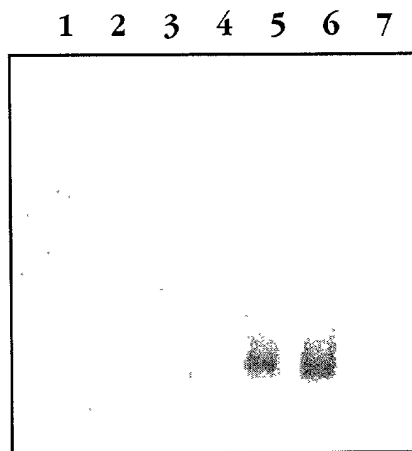


Fig. 5C

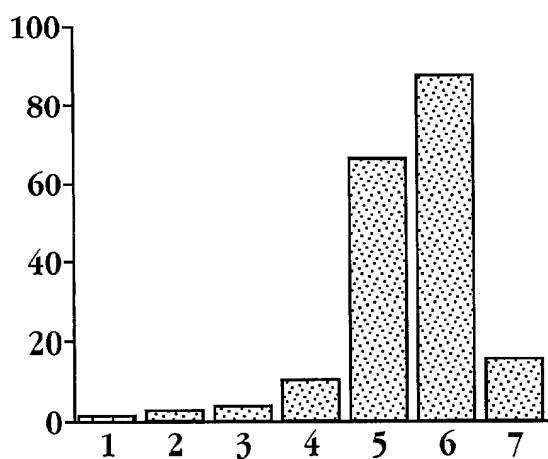


Fig. 5B

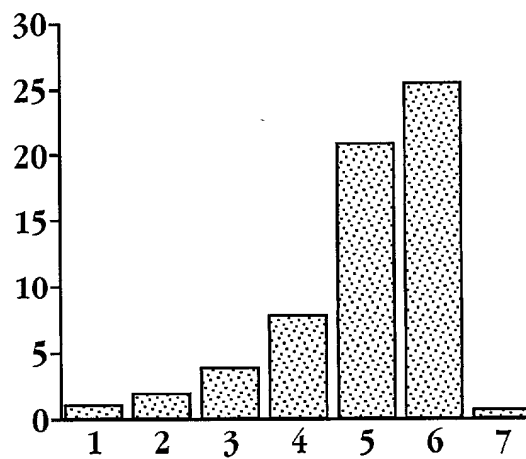


Fig. 5D

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      -968      -958      -948      -938      -928      -918      -908      -898
      *         *         *         *         *         *         *         *
TGGAATTGTG AGGGGATAAC AATTTACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTTGGTACC GAGCTCGGAT
                                                    BamHI>
_____pCR2.1_____>
_____Lac promoter_____>

      -888      -878      -868      -858      -848      -838      -828      -818
      *         *         *         *         *         *         *         *
CCACTAGTAA CGGCCGCCAG TGTGCTGGAA TTGGGCTTAC TATAGGGCAC GCGTGGTCGA CGGCCCGGGC TGGTAAATTT
_____pCR2.1_____>
_____GenomeWalker Adaptor_____>
_____6E_____>

      -808      -798      -788      -778      -768      -758      -748      -738
      *         *         *         *         *         *         *         *
TGAAAAGTTA GGAGATATTT TTTACATATA AGAGATATTT TTTATAATGT AACATTTTTT TTTACTAGACG GTTGAGTCGA
_____6E melon genomic DNA_____>

      -728      -718      -708      -698      -688      -678      -668      -658
      *         *         *         *         *         *         *         *
GTTAGGTAA AGAAAGGAAA ACTATAAAAT AATTTTTAAT TATTAAATAC ATAAACAATA CTTTGTATTC TATATTAATT
_____6E melon genomic DNA_____>

      -648      -638      -628      -618      -608      -598      -588      -578
      *         *         *         *         *         *         *         *
AAAATGACTA TTGAATTGTT AAGATGTAGG TATCTAAGGA CAAGAAGTCT CGAGTTCAAA TCTCAACCT CAAAATATAC
_____6E melon genomic DNA_____>

      -568      -558      -548      -538      -528      -518      -508      -498
      *         *         *         *         *         *         *         *
TGCAAGATAG TAACTAATGA ATTATATTTG ACTAAATCAT GTAGCAAAG AAAATCAAAT TTATCATGTT AAATATGGTC
_____6E melon genomic DNA_____>

      -488      -478      -468      -458      -448      -438      -428      -418
      *         *         *         *         *         *         *         *
AAGCCGGAGC ATTAACAACA ACAATTCATA TTTGTGGTTG ATAGTACTTG ACTAGAATTT AGAGAGTACT TGACTAGAAT
_____6E melon genomic DNA_____>

      -408      -398      -388      -378      -368      -358      -348      -338
      *         *         *         *         *         *         *         *
AAAAATTGGG GGACCCACTA CGACGTCAGC TTGCCTTGCT TAGCAATTAA GCTATCACCT CTTAGTCTAT AGCTTCGTGC
_____6E melon genomic DNA_____>

```

Fig. 6A

box>

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-328      -318      -308      -298      -288      -278      -268      -258
  *        *        *        *        *        *        *        *
GCTGCATTAA ACGGTATTCT CACACTTTTC TTTTCITTTT ACCGCACCCG TCCGGTTAAT GGCTCCCCCA CTTTTTACCT
_____6E melon genomic DNA_____>

-248      -238      -228      -218      -208      -198      -188      -178
  *        *        *        *        *        *        *        *
TCCCCGAATC CACGCCAGTT GCCAACATGC GAAGCAGCAA GTACAATATT GTCATTTTGC ATTAACCAAA ATGACACGTC
_____6E melon genomic DNA_____>

TATA
|
-168      -158      -148      -138      -128      -118      -108      -98
  *        *        *        *        *        *        *        *
GGATGICATT TATGTAATTA AGCTACAAAG CCACGGTTAG TTTCGGAACC CCCACGATCC AGTACTTACG TGTCTCCTAT
_____6E melon genomic DNA_____>

-88      -78      -68      -58      -48      -38      -28      -18
  *        *        *        *        *        *        *        *
AAATCTTAGA AGCAACGTC TACCGGAAT CAACICATTA GGTATCCCAT TTTCATCTAT CAATCACCC TTGAAACTGC
_____6E melon genomic DNA_____>

6E translational start site
|
<6EMelNcoP
-8      1 3      |
  *      * *      |
TTTTCCTGGC ACGACT ATG GCC TC
AAAAGGGCCG aGGCTGg TAC CGG A
--NcoI--
_____6E melon genomic DNA_____

```

Fig. 6B

-2442 -2432 -2422 -2412 -2402 -2392 -2382 -2372
 * * * * * * * *
AAGCTTCAT GOCTGCAGGT CGACTCTAGA TCAATCAAAC ATTATATTAA ATAGAACGTT TTAGTGGTTT TTGGATTITA
 -Hind3
 _____ pUC-19 _____>
 _____ 2F melon genomic DNA _____>

-2362 -2352 -2342 -2332 -2322 -2312 -2302 -2292
 * * * * * * * *
TTTATCTTTT TTATTATTTA CATTCAATTT AGATTTAACT CTTGCAGAAG ATGGAGGAAG AGAATTTTTA GAAATTGAAC
 _____ 2F melon genomic DNA _____>

-2282 -2272 -2262 -2252 -2242 -2232 -2222 -2212
 * * * * * * * *
TGAAATGAGC TTAATTATTA AAAATCAAAA GAAAAATGGT GCCAACAAAG GTGACTAAGA GTGTAATGAA TTGGAATTAG
 _____ 2F melon genomic DNA _____>

-2202 -2192 -2182 -2172 -2162 -2152 -2142 -2132
 * * * * * * * *
AACCTTCCTT CTGTATAGAT ATAATTGATG TTTTCTTAA CTTTATTTTT ATGGTGGTTA TTTATTAATA ACTGAATTTT
 _____ 2F melon genomic DNA _____>

-2122 -2112 -2102 -2092 -2082 -2072 -2062 -2052
 * * * * * * * *
TAAGAGTICT TTTAATAACC AAATGTTATA GGATTCAAIT GATTGTTTTA TGAGATTAGG CAAACACTIT ATATTGGAGA
 _____ 2F melon genomic DNA _____>

-2042 -2032 -2022 -2012 -2002 -1992 -1982 -1972
 * * * * * * * *
AATAATTTAG TGTAGAAAGT AATTTTCATT TTGGATTGTT TAGATGAACA TCAAATCTTG CAACAACATT CAGTTAAGTA
 _____ 2F melon genomic DNA _____>

-1962 -1952 -1942 -1932 -1922 -1912 -1902 -1892
 * * * * * * * *
TATATAAATA TATAGAGCCA CCAACCTCAA ATACAATATC TTCGGAAGCA AAATATTATA CATAATATGG AAAGAAGAGT
 _____ 2F melon genomic DNA _____>

-1882 -1872 -1862 -1852 -1842 -1832 -1822 -1812
 * * * * * * * *
AGTACTGGTA CATGAATCTT ACGAAGAATT TAAGTATTAT TGGCTTTTCC AATGCAGAAG TCTCAACAAA TCACATTTTA
 _____ 2F melon genomic DNA _____>

-1802 -1792 -1782 -1772 -1762 -1752 -1742 -1732
 * * * * * * * *
AAAACCGATT GAATAACAT GCAAGTAAGA CTTTTGAAAA AACAAGCATT CAAACCTCAT ATCAATTATC TCTATATGCA
 _____ 2F melon genomic DNA _____>

-1722 -1712 -1702 -1692 -1682 -1672 -1662 -1652
 * * * * * * * *
AAATGTTAGG TCAAATGAGT AATGAAATTA AGGACAAATC AACTAAAAAG AATCAATAAA GTGAATCGAA AAGAAACAAA
 _____ 2F melon genomic DNA _____>

Fig. 7A

```

-1642      -1632      -1622      -1612      -1602      -1592      -1582      -1572
  *         *         *         *         *         *         *         *
TATCAATCAA ACCTAATGTA TACGTGATIG ATGATGCAGT GIGTTTTGAG ATATGGACAT TTTGATAAAC AACAAACCTC
2F melon genomic DNA>

-1562      -1552      -1542      -1532      -1522      -1512      -1502      -1492
  *         *         *         *         *         *         *         *
CACTCCAATA CGAGAAGAGA GGCATTGAGT GACAGATTAG TGCCCTATTG AAGAGGGTAA GTCCAAAACA AAACAAACAC
2F melon genomic DNA>

-1482      -1472      -1462      -1452      -1442      -1432      -1422      -1412
  *         *         *         *         *         *         *         *
AAAACATGGT GAAGAAATGT TATGAATAAA TGGCAGGGAA AGACATGGTT GTACATGTGG TGTGAGTTTT CTCTTTTCAA
2F melon genomic DNA>

-1402      -1392      -1382      -1372      -1362      -1352      -1342      -1332
  *         *         *         *         *         *         *         *
ATCTGTGAAT AAATTGGATT ACGACCCAAC AAGAGAAACA CTGTTTGAA ACCATGACAG GGCTACCCCA TGGCGTGAAT
2F melon genomic DNA>
-NcoI-

-1322      -1312      -1302      -1292      -1282      -1272      -1262      -1252
  *         *         *         *         *         *         *         *
ATCAAGTATT TAATTAATTA AGCTCTCATC CCGCCATTC GTTTTTTTAT TCGATTCATA TCTTATATTT TATATACGAA
2F melon genomic DNA>

-1242      -1232      -1222      -1212      -1202      -1192      -1182      -1172
  *         *         *         *         *         *         *         *
TAATTCCTGA GTTGATTTC AATTIAGTTC GTCAATAGTA ATATTTTAAA CTATGTTAAT ATATAAAAAG TAAATGCGAA
2F melon genomic DNA>

-1162      -1152      -1142      -1132      -1122      -1112      -1102      -1092
  *         *         *         *         *         *         *         *
TGATTCCTATT AGTATTCACT TTATATCACT CCTTCCTAGA GTAAAGTTTT TAAAGTGGGA AGGGAAATGG AATACGACGT
2F melon genomic DNA>

-1082      -1072      -1062      -1052      -1042      -1032      -1022      -1012
  *         *         *         *         *         *         *         *
GIGATTGGTA GTTAAATTTC CTTATCGACG AGGTACTGT TTCCTTACTT ATATATATGG AGTCATCCTC AATTTTTCAA
2F melon genomic DNA>

-1002      -992      -982      -972      -962      -952      -942      -932
  *         *         *         *         *         *         *         *
CTCTCAACTT CCAATTATAC AAGCAAAACA TTCAATACCA TACATGCATC TTTTTAGAAA GAAAAGAAGT TCTCTCTTGG
2F melon genomic DNA>

-922      -912      -902      -892      -882      -872      -862      -852
  *         *         *         *         *         *         *         *
ACTTTTTTTT TCAATTC AAC TATGCACCTT TGTATTITTA GTTTTATAAT TTTTGTIGTT TCTTCCGTTT AATCAAGTTG
2F melon genomic DNA>

```

Fig. 7B

-842	-832	-822	-812	-802	-792	-782	-772
*	*	*	*	*	*	*	*
TTGTAATCAA	CTTTATGTGAT	TCAAACACAT	AGATATTTTGT	TTTAATAGTA	TCAGTATATA	ATAGGGTTAG	AATAACCTTT
2F melon genomic DNA							
-762	-752	-742	-732	-722	-712	-702	-692
*	*	*	*	*	*	*	*
CAAATATGTG	TTTTTAAAAA	ATCAAATCAC	TTTAAAAAAT	AAAATATGTT	TAATTAGTGT	ATGTTTTTCT	TTTTAAGTAT
2F melon genomic DNA							
-682	-672	-662	-652	-642	-632	-622	-612
*	*	*	*	*	*	*	*
TAAACCACGA	TAAAAAGTGC	TTTAACACTT	ATAAAAAAAT	AGATTAATTT	AAAGGAAGTT	GTCTGAACGG	CAAAATTGAC
2F melon genomic DNA							
-602	-592	-582	-572	-562	-552	-542	-532
*	*	*	*	*	*	*	*
AAAATATAAC	AAAGTTTAAT	GAACATTGTT	CGAAATGTTT	CGAAGAGGAA	AGAAAACATT	AAGTTTGAAA	TATCTCGAGT
2F melon genomic DNA							
-522	-512	-502	-492	-482	-472	-462	-452
*	*	*	*	*	*	*	*
TAAATACATA	TCATCCCATTA	GTAATATATA	ACAAAACAAA	CTTAAATCTG	AAAAAAAAT	TGATGTTAAT	AAGAAAAAGA
2F melon genomic DNA							
-442	-432	-422	-412	-402	-392	-382	-372
*	*	*	*	*	*	*	*
GATCAAACIC	TTAATTTTTT	AAAAAATAA	TGGTGAAAAA	AACTGAAAAT	TTTCCAATAT	TGTTTAATTT	CAAATTGATC
2F melon genomic DNA							
-362	-352	-342	-332	-322	-312	-302	-292
*	*	*	*	*	*	*	*
CAAAAAATTAA	AGTTAAAAAA	GCATTAAACA	AAACAATTCA	AAACCTAGCT	ACTACACATT	TACGAAAATA	TATGATACAC
2F melon genomic DNA							
-282	-272	-262	-252	-242	-232	-222	-212
*	*	*	*	*	*	*	*
AAAGGATTTT	TGGGTGTAAA	CATCTTTTTT	ATTTTATATA	CACCAAACCT	CGTATATATT	CACACATAAA	GAAGGAAAAA
2F melon genomic DNA							
-202	-192	-182	-172	-162	-152	-142	-132
*	*	*	*	*	*	*	*
GAATTAATGC	AAGGGTGTGG	CCAATTACGT	ACCGTCGTCA	TATCTACTC	ATCCGTTACG	TTCTCAAATC	TCTCTCTCTC
2F melon genomic DNA							
-122	-112	-102	-92	-82	-72	-62	-52
*	*	*	*	*	*	*	*
CCTGCTCTCC	TAATTATTTT	TGCCAGCGAC	CATATTTTCAT	TTTCAATTGT	GTGTTTAAAA	AGCCGAGAAT	CGCAATCCTT
2F melon genomic DNA							
Translational start site							
-42	-32	-22	-12	-2			
*	*	*	*	*			
TTTCTCTCCAC	TCTTAATTTCA	TTTCCAATTC	ACAAAAAT	A	G	GATCCGCCAC	CATGG
2F melon genomic DNA							
				-BamHI-	-NcoI-		

Fig. 7C

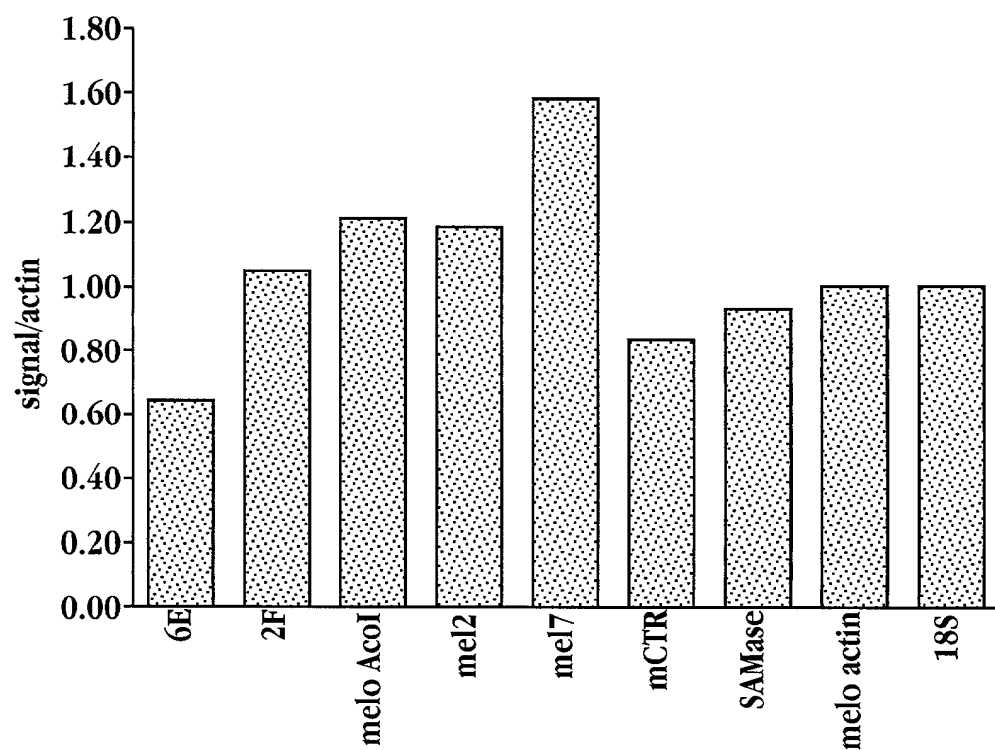


Fig. 8